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        GenCore version 4.5
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OM protein - protein search, using sw model

Run on:    September  8, 2001, 14:39:33 ; Search time 19.61 seconds
                                           (without alignments)
                                           4262.284 Million cell updates/sec

Title:       US-09-522-753-11
Perfect score: 12643
Sequence:    1 MSSSGYPPNQGAFSTEQSRY.........EREPAPLLSAQYETLSDSDD 2440

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched:    93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters:       93435

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
```

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	12643	100.0	2440	1	NCR1_HUMAN	O75376 homo sapien
2	11536.5	91.2	2453	1	NCR1_MOUSE	Q60974 mus musculu
3	4147.5	32.8	2517	1	NCR2_HUMAN	Q9y618 h nuclear r
4	4055.5	32.1	2472	1	NCR2_MOUSE	Q9vu42 mus musculu
5	2493.5	19.7	533	1	NCR1_RAT	Q9wdb5 rattus norv
6	480	3.7	2468	1	MAPB_HUMAN	P46821 homo sapien
7	465.5	3.7	2774	1	MAPA_RAT	P34926 rattus norv
8	447	3.5	2464	1	MAPB_MOUSE	P14873 mus musculu
9	437.5	3.5	2805	1	MAPA_HUMAN	P78559 homo sapien
10	437	3.5	2845	1	APC_MOUSE	Q61315 mus musculu
11	411.5	3.3	3924	1	ANK2_HUMAN	Q01484 homo sapien
12	406	3.2	2842	1	APC_RAT	P70478 rattus norv
13	404	3.2	3256	1	KI67_HUMAN	P46013 homo sapien
14	390	3.1	1226	1	YCS1_YEAST	P25357 saccharomyc
15	374.5	3.0	3562	1	PGCV_CHICK	Q90953 gallus gall
16	365	2.9	2843	1	APC_HUMAN	P25054 homo sapien
17	360	2.8	2349	1	TPR_HUMAN	P12270 homo sapien
18	353	2.8	2142	1	BAT2_HUMAN	P48634 homo sapien
19	350	2.8	661	1	YDBJ_SCHPO	O10369 schizosacch
20	348.5	2.8	1018	1	YK26_CAEEL	P34333 caenorhabdi
21	343.5		1411	1	TCOF_HUMAN	Q13428 homo sapien
22	343	2.7	3866	1	HRX_MOUSE	P55200 mus musculu
23	336	2.7	2688	1	ZEP1_MOUSE	Q03172 mus musculu
24	332.5	2.6	1861	1	MAP2_RAT	P15146 rattus norv
25	326	2.6	1781	1	AKAC_HUMAN	Q02952 homo sapien
26	321.5	2.5	3969	1	HRX_HUMAN	Q03164 homo sapien
27	317	2.5	4687	1	PLE1_RAT	P30427 rattus norv
28	314.5	2.5	3358	1	PGCV_MOUSE	Q62059 mus musculu
29	312	2.5	1902	1	SMF1_HUMAN	O14497 homo sapien
30	310.5	2.5	2004	1	MO2_HUMAN	Q92794 homo sapien
31	309.5	2.4	2441	1	CBP_MOUSE	P45481 mus musculu
32	308	2.4	2442	1	CBE_HUMAN	Q92793 homo sapien
33	303	2.4	3396	1	PGCV_HUMAN	P13611 homo sapien
34	300.5	2.4	2090	1	HFC1_MESAU	P51611 mesocricetu
35	299.5	2.4	2715	1	TRX2_HUMAN	Q9umn6 homo sapien
36	298.5	2.4	771	1	CALD_CHICK	P12957 gallus gall
37	298	2.4	2194	1	SC16_YEAST	P48415 saccharomyc
38	296.5	2.3	1828	1	MAP2_MOUSE	P20357 mus musculu
39	295.5	2.3	848	1	NFM_MOUSE	P08553 mus musculu
40	295	2.3	2035	1	HFC1_HUMAN	P51610 homo sapien
41	295	2.3	2717	1	ZEP1_HUMAN	P15822 homo sapien
42	294	2.3	915	1	NFM_HUMAN	P07197 homo sapien
43	291	2.3	1827	1	MAP2_HUMAN	P11137 homo sapien
44	289	2.3	1637	1	MRSP_STAAU	P80544 staphylococ
45	284.5	2.3	1505	1	CDP_HUMAN	P39880 homo sapien

ALIGNMENTS

```
RESULT  1
NCR1_HUMAN
ID   NCR1_HUMAN     STANDARD;      PRT;   2440 AA.
AC   O75376; Q9UPV5; Q9UO18;
DT   01-OCT-2000 (Rel. 40, Created)
DT   01-OCT-2000 (Rel. 40, Last sequence update)
DT   01-OCT-2000 (Rel. 40, Last annotation update)
DE   NUCLEAR RECEPTOR CO-REPRESSOR 1 (N-COR1) (N-COR).
GN   NCOR1 OR KIAA1047.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Fetal brain;
RX   MEDLINE=98393736; PubMed=9724795;
RA   Wang J., Hoshino T., Redner R.L., Kajigaya S., Liu J.M.;
RT   "ETO, fusion partner in t(8;21) acute myeloid leukemia, represses
RT   transcription by interaction with the human N-CoR/mSin3/HDAC1
RT   complex.";
RL   Proc. Natl. Acad. Sci. U.S.A. 95:10860-10865(1998).
RN   [2]
RP   SEQUENCE OF 782-2440 FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=99397452; PubMed=10470851;
RA   Kikuno R., Nagase T., Ishikawa K.-I., Hirosawa M., Miyajima N.,
RA   Tanaka A., Kotani H., Nomura N., Ohara O.;
RT   "Prediction of the coding sequences of unidentified human genes. XIV.
RT   The complete sequences of 100 new cDNA clones from brain which code
RT   for large proteins in vitro.";
RL   DNA Res. 6:197-205(1999).
RN   [3]
RP   SEQUENCE OF 974-2440 FROM N.A.
RX   MEDLINE=99375328; PubMed=10444336;
RA   Nagaya T., Chen K.-S., Fujieda M., Ohmori S., Richer J.K.,
RA   Horwitz K.B., Lupski J.R., Seo H.;
RT   "Localization of the human nuclear receptor co-repressor (hN-CoR) gene
RT   between the CMT1A and the SMS critical regions of chromosome
RT   17p11.2.";
RL   Genomics 59:339-341(1999).
CC   -!- FUNCTION: MEDIATES THE TRANSCRIPTIONAL REPRESSION ACTIVITY OF SOME
CC       NUCLEAR RECEPTORS BY PROMOTING CHROMATIN CONDENSATION, THUS
CC       PREVENTING ACCESS OF THE BASAL TRANSCRIPTION.
CC   -!- SUBUNIT: FORMS A LARGE COREPRESSOR COMPLEX THAT CONTAINS SIN3A/B
CC       AND HISTONE DEACETYLASES HDAC1 AND HDAC2. THIS COMPLEX ASSOCIATES
CC       WITH THE THYROID (TR) AND THE RETINOID ACID RECEPTORS (RAR) IN THE
CC       ABSENCE OF LIGAND.
CC   -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC   -!- DOMAIN: THE N-TERMINAL REGION CONTAINS REPRESSION FUNCTIONS THAT
CC       ARE DIVIDED INTO THREE INDEPENDANT REPRESSION DOMAINS (RD1, RD2
CC       AND RD3). THE C-TERMINAL REGION CONTAINS THE NUCLEAR RECEPTOR-
CC       INTERACTING DOMAINS THAT ARE DIVIDED IN TWO SEPARATE INTERACTION
CC       DOMAINS (ID1 AND ID2).
CC   -!- DOMAIN: THE TWO INTERACTION DOMAINS (ID) CONTAIN A CONSERVED
CC       SEQUENCE REFERRED TO AS THE CORNR BOX. THIS MOTIF IS REQUIRED AND
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CC      SUFFICIENT TO PERMIT BINDING TO UNLIGANDED TR AND RARS. SEQUENCES
CC      FLANKING THE CORNR BOX DETERMINE NUCLEAR HORMONE RECEPTOR
CC      SPECIFICITY.
CC   -!- SIMILARITY: CONTAINS 1 SANT DOMAIN (COMPOSED OF SANT-A+SANT-B).
CC   -!- SIMILARITY: CONTAINS 2 CORNR BOX.
CC   -!- SIMILARITY: BELONGS TO THE N-COR NUCLEAR RECEPTOR COREPRESSORS
CC      FAMILY.
CC   ------------------------------------------------------
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
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CC      or send an email to license@isb-sib.ch).
CC   ------------------------------------------------------
DR      EMBL; AF044209; AAC33550.1; -.
DR      EMBL; AB028970; BAA82999.1; -.
DR      EMBL; AB019524; BAA75814.1; -.
DR      MIM; 600849; -.
DR      InterPro; IPR001005; -.
DR      Pfam; PF00249; myb_DNA-binding; 2.
DR      PROSITE; PS50090; MYB_3; 1.
KW      Nuclear protein; Transcription regulation; DNA-binding; Repressor;
KW      Coiled coil.
FT      DOMAIN     174    216    COILED COIL (POTENTIAL).
FT      DOMAIN     254    312    INTERACTION WITH SIN3A/B.
FT      DOMAIN     299    328    COILED COIL (POTENTIAL).
FT      DNA_BIND   437    482    SANT-A (POTENTIAL).
FT      DNA_BIND   625    670    SANT-B (POTENTIAL).
FT      DOMAIN     501    557    COILED COIL (POTENTIAL).
FT      DOMAIN     607    617    PRO-RICH.
FT      DOMAIN     988   1816    INTERACTION WITH ETO.
FT      DOMAIN    2055   2059    CORNR BOX OF ID1.
FT      DOMAIN    2263   2267    CORNR BOX OF ID2.
FT      DOMAIN      58     64    POLY-GLN.
FT      DOMAIN     593    603    POLY-ALA.
FT      DOMAIN    1032   1035    POLY-PRO.
FT      DOMAIN    1707   1712    POLY-ALA.
FT      DOMAIN    1952   1963    POLY-SER.
FT      CONFLICT  1014   1014    L -> V (IN REF. 2).
FT      CONFLICT  1508   1509    PP -> SS (IN REF. 2).
FT      CONFLICT  1561   1561    W -> R (IN REF. 2).
FT      CONFLICT  1567   1567    Q -> H (IN REF. 2).
SQ      SEQUENCE 2440 AA;  270263 MW;  60A4D7964D00EDAB CRC64;

Query Match          100.0%;  Score 12643;   DB 1;  Length 2440;
Best Local Similarity 100.0%;  Pred. No. 0:
Matches 2440;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0:

Qy    1 MSSSGYPPNQGAFSTEQSRYPPHSVQYTFPNTRHQQEFAVPDYRSSHLEVSQASQLLQQQ   60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MSSSGYPPNQGAFSTEQSRYPPHSVQYTFPNTRHQQEFAVPDYRSSHLEVSQASQLLQQQ   60

Qy   61 QQQLRRRPSLLSEFHPGSDRPQERRTSYEPFHPGPSPVDHDSLESKRPRLEQVSDSHFQ  120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 QQQLRRRPSLLSEFHPGSDRPQERRTSYEPFHPGPSPVDHDSLESKRPRLEQVSDSHFQ  120

Qy  121 RVSAAVLPLVHPLPEGLRASADAKKDPAFGGKHEAPSSPISGQPCGDDQNASPSKLSKEE  180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 RVSAAVLPLVHPLPEGLRASADAKKDPAFGGKHEAPSSPISGQPCGDDQNASPSKLSKEE  180

Qy  181 LIQSMDRVDREIAKVEQOILKLKKKQQOLEEEAAKPEPEKPVSPPPVEQKHRSIVQIIY  240
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 LIQSMDRVDREIAKVEQOILKLKKKQQOLEEEAAKPEPEKPVSPPPVEQKHRSIVQIIY  240

Qy  241 SENRKKAEEAHKIFEGLGPKVELPLYNQPSDTKVYHENIKTNQVMRKKLILFFKRRNHAR  300
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 DENRKKAEEAHKIFEGLGPKVELPLYNQPSDTKVYHENIKTNQVMRKKLILFFKRRNHAR  300

Qy  301 KQREQKICQRYDQLMEAWEKKVDRIENNPRRKAKESKTREYYEKQFPEIRKQREQQERFQ  360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 KQREQKICQRYDQLMEAWEKKVDRIENNPRRKAKESKTREYYEKQFPEIRKQREQQERFQ  360

Qy  361 RVGQRGAGLSATIARSEHEISEIIDGLSEQENNEKQMRQLSVIPPMWFDAEQRRVKFINM  420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 RVGQRGAGLSATIARSEHEISEIIDGLSEQENNEKQMRQLSVIPPMWFDAEQRRVKFINM  420

Qy  421 NGLMEDPMKVYKDRQFMNVWTDHEKEIFKDKFIQHPKNFGLIASYLERKSVPDCVLYYYL  480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 NGLMEDPMKVYKDRQFMNVWTDHEKEIFKDKFIQHPKNFGLIASYLERKSVPDCVLYYYL  480

Qy  481 TKKNENYKALVRRNYGKRRGRNQQIARPSQEEKVEKEEDKAEKTEKKEEKKDEEEKDE  540
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481 TKKNENYKALVRRNYGKRRGRNQQIARPSQEEKVEKEEDKAEKTEKKEEKKDEEEKDE  540

Qy  541 KEDSKENTKEKDKIDGTAEETEREQATPRGRKTANSQGRRKGRITRSMTNEAAAASAAA  600
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541 KEDSKENTKEKDKIDGTAEETEREQATPRGRKTANSQGRRKGRITRSMTNEAAAASAAA  600

Qy  601 AAATEEPPPLPPPPEPISTEPVETSRWTEEEMEVAKKGLVEHGRNWAAIAKMVGTKSEA  660
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  601 AAATEEPPPLPPPPEPISTEPVETSRWTEEEMEVAKKGLVEHGRNWAAIAKMVGTKSEA  660

Qy  661 QCKNFYFNYKRRHNLDNLLQQHKQKTSRKPREERDVSQCESVASTVSAQEDEDIEASNEE  720
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  661 QCKNFYFNYKRRHNLDNLLQQHKQKTSRKPREERDVSQCESVASTVSAQEDEDIEASNEE  720

Qy  721 ENPEDSEVEAVKPSEDSPENATSRGNTEPAVELEPTTETAPSTSPSLAVPSTKPAEDESV  780
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  721 ENPEDSEVEAVKPSEDSPENATSRGNTEPAVELEPTTETAPSTSPSLAVPSTKPAEDESV  780

Qy  781 ETQVNDSISAETAEQMDVDQQEHSAEEGSVCDPPPATKADSVDVEVRVPENHASKVEGDN  840
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  781 ETQVNDSISAETAEQMDVDQQEHSAEEGSVCDPPPATKADSVDVEVRVPENHASKVEGDN  840

Qy  841 TKERDLDRASEKVEPRDEDLVVAQQINAQRPEPQSDNDSSATCSADEDVDGEPERQRMFP  900
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  841 TKERDLDRASEKVEPRDEDLVVAQQINAQRPEPQSDNDSSATCSADEDVDGEPERQRMFP  900

Qy  901 MDSKPSLLNPTGSILVSSPLKPNPLDLPQLQHRAAVIPPNVSCTPCNIPIGTPVSGYALX  960
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  901 MDSKPSLLNPTGSILVSSPLKPNPLDLPQLQHRAAVIPPNVSCTPCNIPIGTPVSGYALX  960

Qy  961 QRHIKAMHESALLEEQRQREQIDLECRSSTSPCGTSKSPNREWEVLQPAPHQLITNLPE 1020
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  961 QRHIKAMHESALLEEQRQREQIDLECRSSTSPCGTSKSPNREWEVLQPAPHQLITNLPE 1020

Qy 1021 GVRLPTTRRPTRPPPPLIPSSKTTVASEKPSFIMGGSISQGTPGTYLTSHNQASYTQETPK 1080
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1021 GVRLPTTRRPTRPPPPLIPSSKTTVASEKPSFIMGGSISQGTPGTYLTSHNQASYTQETPK 1080

Qy 1081 PSVGSISLGLPRQQEASKSATLPYIKQEEFSPRSONSQPEGLLVRAQHEGVVRGTAGAIQ 1140
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1081 PSVGSISLGLPRQQEASKSATLPYIKQEEFSPRSONSQPEGLLVRAQHEGVVRGTAGAIQ 1140

Qy 1141 EGSITRGTPTSKISVESIPSLRGSTQGTPALPQTGIPTEALVKGSISRMPIEDSSPEKG 1200
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1141 EGSITRGTPTSKISVESIPSLRGSTQGTPALPQTGIPTEALVKGSISRMPIEDSSPEKG 1200

Qy 1201 REEAASKGHVIYEGKSGHILSYDNIKNAREGTRSPRTAHEISLKRSYESVEGNIKQGMSM 1260
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1201 REEAASKGHVIYEGKSGHILSYDNIKNAREGTRSPRTAHEISLKRSYESVEGNIKQGMSM 1260

Qy 1261 RESPVSAPLEGLLCRALPRGSPHSDLKERTVLSGGSIMQGTPRATTESFEDGLKYPKQIKR 1320
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1261 RESPVSAPLEGLLCRALPRGSPHSDLKERTVLSGGSIMQGTPRATTESFEDGLKYPKQIKR 1320

Qy 1321 ESPPIRAFEGAITKGKPYDGITTIKEMGRSIHEIPRQDILTQESRKTPEVVQSTRPIIEG 1380
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1321 ESPPIRAFEGAITKGKPYDGITTIKEMGRSIHEIPRQDILTQESRKTPEVVQSTRPIIEG 1380

Qy 1381 SISQGTPIKFDNNSGQSAIKHNVKSLITGPSKLSRGMPPLEIVPENIKVVERGKYEDVKA 1440
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1381 SISQGTPIKFDNNSGQSAIKHNVKSLITGPSKLSRGMPPLEIVPENIKVVERGKYEDVKA 1440
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Qy.  1441  GETVRSRHTSVVSSGPSVLRSTLHEAPKAQLSPGIYDDTSARRTPVSVQNTMSRGSPMQN  1500
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441  GETVRSRHTSVVSSGPSVLRSTLHEAPKAQLSPGIYDDTSARRTPVSVQNTMSRGSPMQN  1500

Qy   1501  RTSDVTIPPNKSTNHERKSTLFPTQRESIPAKSPVPGVDPVVSHSPFDPHHRGSTAGEVY  1560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501  RTSDVTIPPNKSTNHERKSTLFPTQRESIPAKSPVPGVDPVVSHSPFDPHHRGSTAGEVY  1560

Qy   1561  WSHLPTQLDPAMPFHRALDPAAAAYLFQRQLSPTPGYPSQYQLYAMENTRQTILNDYITS  1620
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561  WSHLPTQLDPAMPFHRALDPAAAAYLFQRQLSPTPGYPSQYQLYAMENTRQTILNDYITS  1620

Qy   1621  QQMQVNLRPDVARGLSPREQPLGLPYPATRGIIDLTNMPPTILVPHPGGTSTPPMDRITY  1680
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621  QQMQVNLRPDVARGLSPREQPLGLPYPATRGIIDLTNMPPTILVPHPGGTSTPPMDRITY  1680

Qy   1681  IPGTQITFPPRPYNSASMSPGHPTHLAAAASAEREREREREREREREIAAASSDLYLRP  1740
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681  IPGTQITFPPRPYNSASMSPGHPTHLAAAASAEREREREREREREREIAAASSDLYLRP  1740

Qy   1741  GSEQPGRPGSHGYVRSPSPSVRTQETMLQQRPSVFQGTNGTSVITPLDPTAQLRIMPLPA  1800
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741  GSEQPGRPGSHGYVRSPSPSVRTQETMLQQRPSVFQGTNGTSVITPLDPTAQLRIMPLPA  1800

Qy   1801  GGPSISQGLPASRYNTAADALAALVDAAASAPQMDVSKTKESKHEAARLEENLRSRSAAV  1860
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801  GGPSISQGLPASRYNTAADALAALVDAAASAPQMDVSKTKESKHEAARLEENLRSRSAAV  1860

Qy   1861  SEQQQLEQKTLEVEKRSVQCLYTSSAFPSGKPQPHSSVVYSEAGKDKGPPPKSRYEEELR  1920
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861  SEQQQLEQKTLEVEKRSVQCLYTSSAFPSGKPQPHSSVVYSEAGKDKGPPPKSRYEEELR  1920

Qy   1921  TRGKTTTAANFIDVIITRQIASDKDARERGSQSDSSSSLSSHRYETPSDAIEVISPAS  1980
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921  TRGKTTTAANFIDVIITRQIASDKDARERGSQSDSSSSLSSHRYETPSDAIEVISPAS  1980

Qy   1981  SPAPPQEKLQTYQPEVVKANQAENDPTRQYEGPLHHYRPQQESPSPQQOLPPSSQAEGMG  2040
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981  SPAPPQEKLQTYQPEVVKANQAENDPTRQYEGPLHHYRPQQESPSPQQQLPPSSQAEGMG  2040

Qy   2041  QVPRTHRLITLADHICQIITQDFEARNQVSSOTPOQPPTSTFQNSPSALVSTPVRTKTSNR  2100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041  QVPRTHRLITLADHICQIITQDFEARNQVSSOTPOQPPTSTFQNSPSALVSTPVRTKTSNR  2100

Qy   2101  YSPESQAQSVHIQRPGSRVSPENLVDKSRGSRPGKSPERSHVSSEPYEPISPQVPVVHE  2160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101  YSPESQAQSVHIQRPGSRVSPENLVDKSRGSRPGKSPERSHVSSEPYEPISPQVPVVHE  2160

Qy   2161  KQDSLLLSQRGAEPAEQRNDARSPGSISYLPSFFTKLENTSPMVKSKKQEIFRKLNSSG  2220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161  KQDSLLLSQRGAEPAEQRNDARSPGSISYLPSFFTKLENTSPMVKSKKQEIFRKLNSSG  2220

Qy   2221  GGDSDMAAAQPGTEIFNLPAVTTSGGSVSSRGHSFADPASNLGLEDIIRKALMGSFDDKVE  2280
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221  GGDSDMAAAQPGTEIFNLPAVTTSGGSVSSRGHSFADPASNLGLEDIIRKALMGSFDDKVE  2280

Qy   2281  DHGVVNSQPMGVVPGTANTSVVTSGETRREEGDPSPHSGGVCKPKLISKSNSRKSKSPIP  2340
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281  DHGVVNSQPMGVVPGTANTSVVTSGETRREEGDPSPHSGGVCKPKLISKSNSRKSKSPIP  2340

Qy   2341  GQGYLGTERPSSVSSVHSEGDYHRQTPGWAWEDRPSSTGSTQFPYNPLTMRMLSSTPPTP  2400
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341  GQGYLGTERPSSVSSVHSEGDYHRQTPGWAWEDRPSSTGSTQFPYNPLTMRMLSSTPPTP  2400

Qy   2401  IACAPSAVNQAAPHQQNRIWEREPAPLLSAQYETLSDSDD  2440
           ||||||||||||||||||||||||||||||||||||||||
Db   2401  IACAPSAVNQAAPHQQNRIWEREPAPLLSAQYETLSDSDD  2440
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RESULT  2
NCR1_MOUSE
ID   NCR1_MOUSE     STANDARD;     PRT;   2453 AA.
AC   Q60974; O60812;
DT   01-OCT-2000 (Rel. 40, Created)
DT   01-OCT-2000 (Rel. 40, Last sequence update)
DT   01-OCT-2000 (Rel. 40, Last annotation update)
DE   NUCLEAR RECEPTOR CO-REPRESSOR 1 (N-COR1) (N-COR) (RETINOID X RECEPTOR
DE   INTERACTING PROTEIN 13) (RIP13)
GN   NCOR1 OR RXRIP13.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).
RC   TISSUE=Pituitary;
RX   MEDLINE=96008539; PubMed=7566114;
RA   Hoerlein A.J., Naeaer A.M., Heinzel T., Torchia J., Gloss B.,
RA   Kurokawa R., Ryan A., Kamel Y., Soederstroem M., Glass C.K.,
RA   Rosenfeld M.G.;
RT   "Ligand-independent repression by the thyroid hormone receptor
RT   mediated by a nuclear receptor co-repressor.";
RL   Nature 377:397-404(1995).
RN   [2]
RP   SEQUENCE OF 1792-2453 FROM N.A. (ISOFORM LONG).
RC   TISSUE=Liver;
RX   MEDLINE=95280959; PubMed=7760852;
RA   Seol W., Choi H.S., Moore D.D.;
RT   "Isolation of proteins that interact specifically with the retinoid X
RT   receptor: two novel orphan receptors.";
RL   Mol. Endocrinol. 9:72-85(1995).
CC   -!- FUNCTION: MEDIATES THE TRANSCRIPTIONAL REPRESSION ACTIVITY OF SOME
CC       NUCLEAR RECEPTORS BY PROMOTING CHROMATIN CONDENSATION, THUS
CC       PREVENTING ACCESS OF THE BASAL TRANSCRIPTION.
CC   -!- SUBUNIT: FORMS A LARGE COREPRESSOR COMPLEX THAT CONTAINS SIN3A/B
CC       AND HISTONE DEACETYLASES HDAC1 AND HDAC2. THIS COMPLEX ASSOCIATES
CC       WITH THE THYROID (TR) AND THE RETINOID ACID RECEPTORS (RAR) IN THE
CC       ABSENCE OF LIGAND.
CC   -!- SUBCELLULAR LOCATION: NUCLEAR.
CC   -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS: A LONG FORM (SHOWN HERE) AND A
CC       SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC   -!- TISSUE SPECIFICITY: UBIQUITOUS.
CC   -!- DOMAIN: THE N-TERMINAL REGION CONTAINS REPRESSION FUNCTIONS THAT
CC       ARE DIVIDED INTO THREE INDEPENDANT REPRESSION DOMAINS (RD1, RD2
CC       AND RD3). THE C-TERMINAL REGION CONTAINS THE NUCLEAR RECEPTOR-
CC       INTERACTING DOMAINS THAT ARE DIVIDED IN TWO SEPARATE INTERACTION
CC       DOMAINS (ID1 AND ID2).
CC   -!- DOMAIN: THE TWO INTERACTION DOMAINS (ID) CONTAIN A CONSERVED
CC       SEQUENCE REFERRED TO AS THE CORNR BOX. THIS MOTIF IS REQUIRED AND
CC       SUFFICIENT TO PERMIT BINDING TO UNLIGANDED TR AND RARS. SEQUENCES
CC       FLANKING THE CORNR BOX DETERMINE NUCLEAR HORMONE RECEPTOR
CC       SPECIFICITY.
CC   -!- SIMILARITY: CONTAINS 1 SANT DOMAIN (COMPOSED OF SANT-A+SANT-B).
CC   -!- SIMILARITY: CONTAINS 2 CORNR BOX.
CC   -!- SIMILARITY: BELONGS TO THE N-COR NUCLEAR RECEPTOR COREPRESSORS
CC       FAMILY.
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DR   EMBL; U35312; AAB17125.1; -.
DR   EMBL; U22016; AAC52168.1; -.
DR   MGD; MGI:1349717; Ncor1.
DR   InterPro; IPR01005; -.
DR   Pfam; PF00249; myb_DNA-binding; 2.
DR   PROSITE; PS50090; MYB_3; 1.
KW   Nuclear protein; Transcription regulation; DNA-binding; Repressor;
KW   Coiled coil; Alternative splicing.
FT   DOMAIN        174    216       COILED COIL (POTENTIAL).
FT   DOMAIN        254    312       INTERACTION WITH SIN3A/B (BY SIMILARITY).
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